[SEQUENCE LISTING]

<110> Genomine, Inc.
POSTECH FOUNDATION

<120> Novel phytochrome-interacting protein and a use thereof

<130> OP05-1002

<150> KR 10-2004-0013663
<151> 2004-02-27

<160> 15

<170> KopatentIn 1.71

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<220>
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ctcgagctac ttgtttgctg cagcgagttc 30

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<212> DNA
<213> Arabidopsis thaliana

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gaactcaaca gcaacaacgc tgtgtattgg gcaaatcgtg catttgctca cacaaaactg 180

gaggaatatg gcagtgcaat acaggatgca tcgaaggcca ttgaagttga ttcaagatac 240

tctaagggct attacaggcg tggtgctgcg tatcttgcca tgggaaaatt taaggatgcc 300

ttgaaggact tccaacaggt aaaaaggctt tctcctaatg accctgatgc cacaagaaag 360

ctaaaggaat gtgagaaagc agtgatgaaa ctcaaatttg aagaagcaat ctctgtgcca 420

gtatctgaaa ggcgttcagt agctgagtcc attgacttcc atacaataga ggttgagcca 480

caatattctg gtgctagaat tgagggagag gaagttacct tagattttgt gaaaacgatg 540

atggaggatt ttaagaacca aaaaacattg cataaacggt atgcctatca aatcgtctta 600

cagactaggc aaatcttgct agcactgcct tctcttgttg atataagtgt tccacatggc 660

aaacatatca ctgtttgcgg tgacgttcat ggtcagttct acgatcttct caatatcttt 720

gagcttaatg gcctcccttc ggaggagaac ccatacctat ttaatggcga ctttgtggac 780

agaggctcat tctccgttga gatcatcctc actttgtttg ctttcaagtg catgtgccca 840

tcatccatat atctagccag aggaaaccat gaaagcaaga gcatgaacaa aatttatggt 900

tttgagggtg aggttcggtc caagttgagt gaaaaattcg tggatctctt tgctgaagtt 960

ttctgttacc tcccgttggc tcatgttata aatgggaagg tcttcgtggt acatggaggt 1020

cttttcagtg ttgacggcgt gaaactctca gacatcagag ccattgacag attctgtgag 1080

ccaccagagg aaggactaat gtgtgaacta ttgtggagtg atcctcaacc tctccctgga 1140

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<211> 484
<212> PRT
<213> Arabidopsis thaliana

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Lys Ser Gln Ala Asn Glu Ala Phe Lys Gly His Lys Tyr Ser Ser Ala
20 25 30

Ile Asp Leu Tyr Thr Lys Ala Ile Glu Leu Asn Ser Asn Asn Ala Val
35 40 45

Tyr Trp Ala Asn Arg Ala Phe Ala His Thr Lys Leu Glu Glu Tyr Gly
50 55 60

Ser Ala Ile Gln Asp Ala Ser Lys Ala Ile Glu Val Asp Ser Arg Tyr
65 70 75 80

Ser Lys Gly Tyr Tyr Arg Arg Gly Ala Ala Tyr Leu Ala Met Gly Lys
85 90 95

Phe Lys Asp Ala Leu Lys Asp Phe Gln Gln Val Lys Arg Leu Ser Pro
100 105 110

Asn Asp Pro Asp Ala Thr Arg Lys Leu Lys Glu Cys Glu Lys Ala Val
115 120 125

Met Lys Leu Lys Phe Glu Glu Ala Ile Ser Val Pro Val Ser Glu Arg
130 135 140

Arg Ser Val Ala Glu Ser Ile Asp Phe His Thr Ile Glu Val Glu Pro
145 150 155 160

Gln Tyr Ser Gly Ala Arg Ile Glu Gly Glu Glu Val Thr Leu Asp Phe
165 170 175

Val Lys Thr Met Met Glu Asp Phe Lys Asn Gln Lys Thr Leu His Lys
180 185 190

Arg Tyr Ala Tyr Gln Ile Val Leu Gln Thr Arg Gln Ile Leu Leu Ala
195 200 205

Leu Pro Ser Leu Val Asp Ile Ser Val Pro His Gly Lys His Ile Thr
210 215 220

Val Cys Gly Asp Val His Gly Gln Phe Tyr Asp Leu Leu Asn Ile Phe
225 230 235 240

Glu Leu Asn Gly Leu Pro Ser Glu Glu Asn Pro Tyr Leu Phe Asn Gly
245 250 255

Asp Phe Val Asp Arg Gly Ser Phe Ser Val Glu Ile Ile Leu Thr Leu
260 265 270

Phe Ala Phe Lys Cys Met Cys Pro Ser Ser Ile Tyr Leu Ala Arg Gly
275 280 285

Asn His Glu Ser Lys Ser Met Asn Lys Ile Tyr Gly Phe Glu Gly Glu
290 295 300

Val Arg Ser Lys Leu Ser Glu Lys Phe Val Asp Leu Phe Ala Glu Val
305 310 315 320

Phe Cys Tyr Leu Pro Leu Ala His Val Ile Asn Gly Lys Val Phe Val
325 330 335

Val His Gly Gly Leu Phe Ser Val Asp Gly Val Lys Leu Ser Asp Ile
340 345 350

Arg Ala Ile Asp Arg Phe Cys Glu Pro Pro Glu Glu Gly Leu Met Cys
355 360 365

Glu Leu Leu Trp Ser Asp Pro Gln Pro Leu Pro Gly Arg Gly Pro Ser
370 375 380

Lys Arg Gly Val Gly Leu Ser Phe Gly Gly Asp Val Thr Lys Arg Phe
385 390 395 400

Leu Gln Asp Asn Asn Leu Asp Leu Leu Val Arg Ser His Glu Val Lys
405 410 415

Asp Glu Gly Tyr Glu Val Glu His Asp Gly Lys Leu Ile Thr Val Phe
420 425 430

Ser Ala Pro Asn Tyr Cys Asp Gln Met Gly Asn Lys Gly Ala Phe Ile
435 440 445

Arg Phe Glu Ala Pro Asp Met Lys Pro Asn Ile Val Thr Phe Ser Ala
450 455 460

Val Pro His Pro Asp Val Lys Pro Met Ala Tyr Ala Asn Asn Phe Leu
465 470 475 480

Arg Met Phe Asn

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<400> 6
ctcgagttag ttgaacatcc tgag 24

<210> 7
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<400> 7

ggatccgatg tcaggctcta ggccgact 28

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<220>
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ctcgagtcaa gagattgctt cttcaaa 27

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ggatccatgc cagtatctga aaggcgt 27

<210> 12
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<400> 12
atggagacca agaatgagaa ttct 24

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ttagttgaac atcctgagaa agtt 24

<210> 14
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<212> PRT
<213> Arabidopsis thaliana
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His Thr Ile Glu Val Glu Pro Gln Tyr Ser Gly Ala Arg Ile Glu Gly
20 25 30

Glu Glu Val Thr Leu Asp Phe Val Lys Thr Met Met Glu Asp Phe Lys
35 40 45

Asn Gln Lys Thr Leu His Lys Arg Tyr Ala Tyr Gln Ile Val Leu Gln
50 55 60

Thr Arg Gln Ile Leu Leu Ala Leu Pro Ser Leu Val Asp Ile Ser Val
65 70 75 80

Pro His Gly Lys His Ile Thr Val Cys Gly Asp Val His Gly Gln Phe
85 90 95

Tyr Asp Leu Leu Asn Ile Phe Glu Leu Asn Gly Leu Pro Ser Glu Glu
100 105 110

Asn Pro Tyr Leu Phe Asn Gly Asp Phe Val Asp Arg Gly Ser Phe Ser
115 120 125

Val Glu Ile Ile Leu Thr Leu Phe Ala Phe Lys Cys Met Cys Pro Ser
130 135 140

Ser Ile Tyr Leu Ala Arg Gly Asn His Glu Ser Lys Ser Met Asn Lys
145 150 155 160

Ile Tyr Gly Phe Glu Gly Glu Val Arg Ser Lys Leu Ser Glu Lys Phe
165 170 175

Val Asp Leu Phe Ala Glu Val Phe Cys Tyr Leu Pro Leu Ala His Val
180 185 190

Ile Asn Gly Lys Val Phe Val Val His Gly Gly Leu Phe Ser Val Asp
195 200 205

Gly Val Lys Leu Ser Asp Ile Arg Ala Ile Asp Arg Phe Cys Glu Pro
210 215 220

Pro Glu Glu Gly Leu Met Cys Glu Leu Leu Trp Ser Asp Pro Gln Pro
225 230 235 240

Leu Pro Gly Arg Gly Pro Ser Lys Arg Gly Val Gly Leu Ser Phe Gly
245 250 255

Gly Asp Val Thr Lys Arg Phe Leu Gln Asp Asn Asn Leu Asp Leu Leu
260 265 270

Val Arg Ser His Glu Val Lys Asp Glu Gly Tyr Glu Val Glu His Asp
275 280 285

Gly Lys Leu Ile Thr Val Phe Ser Ala Pro Asn Tyr Cys Asp Gln Met

290 295 300

Gly Asn Lys Gly Ala Phe Ile Arg Phe Glu Ala Pro Asp Met Lys Pro
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Asn Ile Val Thr Phe Ser Ala Val Pro His Pro Asp Val Lys Pro Met
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Ala Tyr Ala Asn Asn Phe Leu Arg Met Phe Asn
340 345

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acgatgatgg aggattttaa gaaccaaaaa acattgcata aacggtatgc ctatcaaatc 180

gtcttacaga ctaggcaaat cttgctagca ctgccttctc ttgttgatat aagtgttcca 240

catggcaaac atatcactgt ttgcggtgac gttcatggtc agttctacga tcttctcaat 300

atctttgagc ttaatggcct cccttcggag gagaacccat acctatttaa tggcgacttt 360

gtggacagag gctcattctc cgttgagatc atcctcactt tgtttgcttt caagtgcatg 420

tgcccatcat ccatatatct agccagagga aaccatgaaa gcaagagcat gaacaaaatt 480

tatggttttg agggtgaggt tcggtccaag ttgagtgaaa aattcgtgga tctctttgct 540

gaagttttct gttacctccc gttggctcat gttataaatg ggaaggtctt cgtggtacat 600

ggaggtcttt tcagtgttga cggcgtgaaa ctctcagaca tcagagccat tgacagattc 660

tgtgagccac cagaggaagg actaatgtgt gaactattgt ggagtgatcc tcaacctctc 720

cctggaagag gcccaagcaa gcgaggagtt ggtctatcat ttggtggaga tgtgacaaag 780

aggtttttgc aagataacaa tttagatttg ttggtccggt cacatgaagt aaaagatgaa 840

ggttatgagg ttgaacatga cggtaaactc ataactgtct tctctgcgcc aaattactgt 900

gatcagatgg gtaataaggg agccttcatt cgttttgaag ctcctgatat gaagccaaac 960

attgttacat tctcagcagt gcctcatccg gatgtgaagc ctatggcata tgcaaacaac 1020

tttctcagga tgttcaacta a 1041